

TITLE Plant transcription factors and enhanced gene expression

expression

expression

GenCore version 5.1.6
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OK: nucleic - nucleic search, using sw model

Run on: September 12, 2003, 20:17:06 | Search time 119.982 seconds

(without alignments) 16178.155 Million cell updates/sec

Title: US-09-847-232a-26

Perfect score: 779 847-232a-26

Sequence: 1 tctctgtatgagcgaacac.....tctatctatctacgaacac 779

Scoring table: IDENTITY-MSC

Coverage 10.0 / Expect 1.0

Searched: 2557256 seqs, 1349715017 residues

Total number of hits satisfying chosen parameters: 510513

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries |

Database: 1: /SIDSI/seqdata/geneseq/geneseq-emb/NA1980.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	ID	Description
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2	779	100.0	779	AA005226	Rice glutein 1/GC
3	749.8	96.3	1488	AF192331	Glutelin promoter
4	707	90.8	4505	24 AA18432	Pleatid p4246 en
5	706	90.6	786	AA043198	Rice GLT (glutelin
6	706	90.6	786	24 AA065525	Rice glutelin (GLT)
7	689	88.4	4227	24 AA18425	Pleatid p4246 en

9	689	88.4	4655	24 AA18420	Pleatid p4246 en
10	689	88.4	5355	24 AA18423	Pleatid p4245 en
11	688	88.3	650	24 AA18415	Gr-1 promoter poly
12	684.4	10.8	839	24 AA15312	Gr-1 promoter DRK
13	84.4	10.8	839	24 AA15312	Gr-1 promoter DRK
14	84.4	10.8	839	24 AA15312	Gr-1 promoter DRK
15	48	6.2	6120	22 AA51788	Tumor suppressor
16	47.2	6.1	85	24 AA15214	Gr-1 signal peptide
17	47.2	6.1	85	24 AA15214	Gr-1 signal peptide
18	47.2	6.1	85	24 AA15214	Gr-1 signal peptide
19	47.2	6.1	85	24 AA15214	Gr-1 signal peptide
20	43.8	5.6	2889	22 AA12954	Drosophila salivary
21	43.8	5.6	2889	22 AA12954	Drosophila salivary
22	41.4	5.3	5508	24 AA13398	Human immune system
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25	40.8	5.2	150841	24 AA00100	Human neutrophil-1
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28	40.8	5.2	150841	24 AA00100	Human neutrophil-1
29	40	5.1	53	24 AA18443	Gr-1 promoter
30	40	5.1	53	24 AA18443	Gr-1 promoter
31	39.6	5.1	6880	24 AA51222	Signal transduction
32	39.6	5.1	6880	24 AA51222	Signal transduction
33	39.6	5.1	6880	24 AA51222	Signal transduction
34	39.6	5.1	6880	24 AA51222	Signal transduction
35	39.2	5.0	7773	24 AA13397	Human immune system
36	39.2	5.0	11745	24 AA02311	DNA transfection
37	39.2	5.0	11745	24 AA02311	DNA transfection
38	39	5.0	2000	24 AA21612	Human reproductive
39	39	5.0	2000	24 AA21612	Human reproductive
40	39	5.0	3104	22 AA10568	Human ovary and
41	39	5.0	3104	22 AA10568	Human ovary and
42	38.6	5.0	7110	24 AA10568	Tumor suppressor
43	38.6	5.0	7110	24 AA10568	Tumor suppressor
44	38.6	5.0	7110	24 AA10568	Tumor suppressor
45	38.6	5.0	7110	24 AA10568	Tumor suppressor

ALIGNMENTS

RESULTS 1
ID AA005226 standard: DRK, 779 BP.
CX AA005226

20-FEB-2002 (first entry)

Rice glutein 1/GC1 upstream regulatory sequence SEQ ID NO 26.

DE Gene expression, Rice: corn, hairy, wheat; transfection factor; FF
KW seed-specific promoter; transgenic plant; O2; Opuntia 2; FBF; GLT
RV Globulin; BKF; cereal; maize; ds.

OX Oryza sativa

FX WC00018795-M2.

XX 08-MAY-2001.

PF 02-MAY-2001; 2001NOV-0514234.

FR 02-MAY-2001; 2001NOV-0514234.

FX 06-FEB-2001; 2001NOV-0514234.

FX (PRTT) APFLATED PRYTHOGENICS INC.

XX Huang N, Peng Y, Tang D, Schmidt EJ

WP; 2002-041504/05.

COMMENT

Identification of this BAC-end sequence was carried out as part of a collaboration with the Russian group of Dr. Boris Pavlov (Pavlov Institute - <http://www.adsp.ac.uk>). This Dirosophila melanogaster BAC-end library (DrosBAC) was made by Alain Billard at CERN (Centre National de la Recherche Scientifique) as part of a large-scale project grant. The DNA was prepared from embryos of a 1st instar and Gevelote Paris. It has been constructed in the vector pUC19.

FEATURES

Source

1. 802

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DB

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443 AAAAGGAGAGCTTATAGACAAAGGCTGACTGACCAAAANTTCACTGCCCTTCGTGTC 502

658 AATCGGATACCAAAATTCAAAATTTAATGCGATTGGTCATCGATCTACGTCCA 717

503 AAAAGACGACGGCTTACACTATTCCTGTGATATTGCAAGGAAGGAGAAACACAA 562

DB 718 TAAAGGAGTGAATATCTACCTAAATATGAGCTCAAAATCTCAGAGGAGAACCACTT 777

63 CA 564

$$770 \pm 770$$

Search completed: September 14, 2003, 02:23:38
Job time : 39.8026 secs

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search completed: success
Job time : 39.8026 secs
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; LENGTH: 4010
; TYPED: 1000
; ORGANISM: Glycine max
US-10-268-754-3

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Matches 88; Conservative 0; Mismatches 77; Idents 0; Gaps 0;

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07 411 CATAAATCTCGAGAGCTATATGTCATATGCAAAATGATGTAAGCAAGCA 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
07 471 ATGCTCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 315 TATTAAGCGTAACTACAGTAACTCAAGCTCAAGATGAAGCAAAATGATGTA 271
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Search completed: September 14, 2003, 07:21:44
 Job time: 134.126 secs

Gencode version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sv model

Run on: September 12, 2003, 20:29:06, Search time 1935.6 seconds

Database: Genbank, 17056,227 million cell updates/sec

Query: us-09-847-232a-35

Perfect score: (6227)

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Scoring table: JNTERVIEW.MSC

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result	Score	Match	Depth	DB ID	Description
1	6227	100.0	6227	AF298122	Sequence 35 from Patent WO081792.
2	6227	100.0	6227	AF298122	Sequence 35 from Patent WO081792.
3	5692.5	91.4	151419	AC093713	AC093713 Oryza sat
4	4695.2	74.8	3564	AB073929	AB073929 Oryza sat
5	4695.2	74.8	3564	AB073929	AB073929 Oryza sat
6	563.4	9.0	1696	R1C827PA	R1C827PA Oryza sat
7	240.2	6.5	4027	R1C827PA	R1C827PA Oryza sat
8	266.8	4.3	1550	R1C827PA	R1C827PA Oryza sat
9	244	3.9	1696	R1C827PA	R1C827PA Oryza sat
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14	173.4	2.8	152343	AC134928	AC134928 Oryza sat
15	173.4	2.8	152343	AC134928	AC134928 Oryza sat
16	162	2.9	102428	AF000510	AF000510 Oryza sat
17	162	2.9	102428	AF000510	AF000510 Oryza sat
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31	158	2.5	144280	AC134927	AC134927 Oryza sat
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34	148	2.4	134014	AC137698	AC137698 Oryza sat
35	146.2	2.3	157172	AC108499	AC108499 Oryza sat
36	146.2	2.3	157172	AC108499	AC108499 Oryza sat
37	144.2	2.3	162536	AB005485	AB005485 Oryza sat
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45	137.4	2.2	10509	AB090485	AB090485 Oryza sat

ALIGNMENTS

Result	Score	Match	Depth	DB ID	Description
1	6227	100.0	6227	AF298122	Sequence 35 from Patent WO081792.
2	6227	100.0	6227	AF298122	Sequence 35 from Patent WO081792.
3	5692.5	91.4	151419	AC093713	AC093713 Oryza sat
4	4695.2	74.8	3564	AB073929	AB073929 Oryza sat
5	4695.2	74.8	3564	AB073929	AB073929 Oryza sat
6	563.4	9.0	1696	R1C827PA	R1C827PA Oryza sat
7	240.2	6.5	4027	R1C827PA	R1C827PA Oryza sat
8	266.8	4.3	1550	R1C827PA	R1C827PA Oryza sat
9	244	3.9	1696	R1C827PA	R1C827PA Oryza sat
10	189.2	3.0	10892	U000000	U000000 Oryza sat
11	189.2	3.0	10892	U000000	U000000 Oryza sat
12	177.8	2.9	159749	AF000020	AF000020 Oryza sat
13	177.8	2.9	159749	AF000020	AF000020 Oryza sat
14	173.4	2.8	152343	AC134928	AC134928 Oryza sat
15	173.4	2.8	152343	AC134928	AC134928 Oryza sat
16	162	2.9	102428	AF000510	AF000510 Oryza sat
17	162	2.9	102428	AF000510	AF000510 Oryza sat
18	162	2.9	102428	AF000510	AF000510 Oryza sat
19	162	2.9	102428	AF000510	AF000510 Oryza sat
20	160.6	2.6	6335	AB034375	AB034375 Oryza sat
21	160.6	2.6	6335	AB034375	AB034375 Oryza sat
22	160.6	2.6	6335	AB034375	AB034375 Oryza sat
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24	159.8	2.6	159920	AF003584	AF003584 Oryza sat
25	159.8	2.6	159920	AF003584	AF003584 Oryza sat
26	159.8	2.6	159920	AF003584	AF003584 Oryza sat
27	159.8	2.6	159920	AF003584	AF003584 Oryza sat
28	158	2.5	144280	AC134927	AC134927 Oryza sat
29	158	2.5	144280	AC134927	AC134927 Oryza sat
30	158	2.5	144280	AC134927	AC134927 Oryza sat
31	158	2.5	144280	AC134927	AC134927 Oryza sat
32	148	2.4	134014	AC137698	AC137698 Oryza sat
33	148	2.4	134014	AC137698	AC137698 Oryza sat
34	148	2.4	134014	AC137698	AC137698 Oryza sat
35	146.2	2.3	157172	AC108499	AC108499 Oryza sat
36	146.2	2.3	157172	AC108499	AC108499 Oryza sat
37	144.2	2.3	162536	AB005485	AB005485 Oryza sat
38	144.2	2.3	162536	AB005485	AB005485 Oryza sat
39	144	2.3	2000	AX556035	AX556035 Sequence
40	143.4	2.3	159193	AF004472	AF004472 Oryza sat
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43	138.8	2.2	1768	AB053472	AB053472 Oryza sat
44	138.4	2.2	115014	AC134795	AC134795 Oryza sat
45	137.4	2.2	10509	AB090485	AB090485 Oryza sat

APPEARANCE: Huang N., Wang Y.S., Yang D., and Schmidt R.J.
FUNCTIONS: Plant transcription factors and enhanced gene expression


```

3181 CTTCTGTTGAGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3440
3182 TTTTCTGTTGAGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3441
3183 CTTCTGTTGAGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3442
3241 GGGGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3400
3242 GGGGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3401
3243 GGGGACATGGGACATATGAGACAGCTGCTACCTGATCTAAACAGCTTAACT 3402
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Authors: Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Title: Submitted (06-Dec-2000) Takaji Sasaki, National Institute of
 Journal: Physiological Sciences, Tokyo Genome Research Program; Kunitomi
 (E-mail:tsasaki@niss.ac.jp, URL: http://rtp.dna.affrc.go.jp/
 Tel:81-298-38-7441, Fax:81-298-38-7460)

COMMENT

This sequence was predicted from the cDNA sequence of a cDNA library (October 1999 version). The genomic sequence was searched against GENCODE 0.0, BLASTX 0.0, BLASTZ 0.0 as well as Splice-Predictor (http://dnh.dna.affrc.go.jp/blast/) and the cDNA sequence database at NCBI. Nonredundant protein database with BLASTP 0.0. ESTs represent corresponding DNA accession no. and RFLP clone ID.
 A gene with identity or significant homology to a protein is classified as a "putative" protein. A gene with identity or significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an "almost" protein. A gene with identity or significant homology to a protein is classified as a "hypothetical" protein. gene prediction program The classification of the sequence is from 98 to 97 of the PNC clone. (DMSJ-A005010) clone at the position 52,821,983-51,561. The sequence of this clone starts at the position 52,986 of the cDNA sequence of this sequence. This sequence of P049812 clone has an overlap with of 37 and the sequence of this clone ends at the position 115 of P051001. Detailed information on overlap and assembly quality Map: with annotation of this entry is available at <http://rtp.dna.affrc.go.jp/genome/blast/>.

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